Amendments to the Claims

Claim 1 (Original): An oligonucleotide sequence which encodes a synthetic suppressor tRNA comprising:

A) a human tRNA structural gene sequence comprising no more than twenty 3' flanking residues and no 5' flanking residues, said sequence encoding an anticodon region for pairing with mRNA;

B) a total length of less than 150 nucleotides;

C) an anticodon sequence which has been modified to recognize a codon different from that which is originally recognized.

Claim 2 (Original): A synthetic suppressor tRNA molecule encoded by the oligonucleotide of claim 1.

Claim 3 (Original): The oligonucleotide of claim 1 wherein said anticodon region encodes an nonsense mutation selected from the group consisting of:
amber (TAG), ochre (UAA) and opal (UGA).

Claim 4 (Original): The oligonucleotide of claim 1 further comprising a second oligonucleotide sequence as described in claim 1 wherein said two sequences are in tandem.

Claim 5 (Original): The oligonucleotide of claim 1 wherein said tRNA structural gene sequence encodes a serine tRNA.

Claim 6 (Original): The oligonucleotide sequence of claim 1 wherein said tRNA structural gene sequence encodes an arginine tRNA.

Claim 7 (Currently amended) ~~The~~ An oligonucleotide ~~of claim 1~~ which encodes a synthetic suppressor tRNA comprising:

A) a human tRNA structural gene sequence comprising no more than twenty 3' flanking residues and no 5' flanking residues, said sequence encoding an anticodon region for pairing with mRNA;

B) a total length of less than 150 nucleotides;

C) an anticodon sequence which has been modified to recognize a codon different from that which is originally recognized;

wherein said oligonucleotide has a sequence selected from the group consisting of SEQ ID NOS:1-10, their complements ~~and their functional equivalents~~.

Claim 8 (Original): A method of restoring translation to a nucleotide sequence which includes a nonsense mutation in a cell comprising:

introducing to said cell a nucleic acid sequence which encodes a synthetic suppressor tRNA oligonucleotide, said oligonucleotide comprising:

A) a human tRNA structural gene sequence comprising no more than twenty 3' flanking residues and no 5' flanking residues, said sequence encoding an anticodon region for pairing with mRNA;

B) a total length of less than 150 nucleotides;

C) an anticodon sequence which has been modified to recognize a codon different from that which is originally recognized, wherein said anticodon is one which will pair with said nonsense mutation and said tRNA structural gene sequence encodes an amino acid which is deleted by said nonsense mutation.

Claim 9 (Original): The method of claim 8 wherein said nucleotide sequence with said nonsense mutation is one which has been introduced to said cell.

Claim 10 (Currently amended): The methodoligonucleotide of claim 8 wherein said tRNA structural gene sequence encodes a serine tRNA.

Claim 11 (Currently amended): The ~~oligonucleotide sequence~~ method of the oligonucleotide claim 8 wherein said tRNA structural gene sequence encodes an arginine tRNA.

Claim 12 (Currently amended): The ~~oligonucleotide~~ method of claim 8 wherein said oligonucleotide has a sequence selected from the group consisting of SEQ ID NOS:1-10, their complements ~~and their functional equivalents~~.

Claim 13 (Original): A method of restoring translation to a nucleotide sequence which includes a nonsense mutation in a cell comprising:

introducing to said cell a synthetic suppressor tRNA oligonucleotide, said oligonucleotide being one which is encoded by the sequence of claim 1.

Claim 14 (Original): A nucleotide vector comprising the nucleotide sequence of claim 1.

Claim 15 (Original): The nucleotide vector of claim 14 wherein said vector is a viral vector.

Claim 16 (Original): The vector of claim 14 wherein said vector is a viral vector selected from the group consisting of:

a retroviral, adenoviral, adeno-associated, Herpes simplex virus and Herpes simplex viral vector.

Claim 17 (Original): The method of claim 14 wherein said vector is a Herpes virus vector.

Claim 18 (Original): The method of claim 14 wherein said vector is a Herpes virus mini amplicon vector comprising:

an Epstein-Barr virus ori P and EBNA-1 sequence to maintain the plasmid episomally, a hygromycin resistance gene, an HSV-1 lytic replication origin (ori S), and a HSV-1 terminal packaging signal.

Claim 19 (Original): The vector of claim 14 wherein said vector is the pH*hargsup* $tRNA^{Opal}$ vector.

Claim 20 (Original): A transformed host cell comprising the nucleotide sequence of claim 1.

Claim 21 (Original): A transformed host cell comprising the synthetic suppressor tRNA molecule of claim 2.

Claim 22 (Original): A method for introducing site-specific mutation to a translated protein comprising:

introducing to said cell a nucleic acid sequence which encodes a synthetic suppressor tRNA oligonucleotide, said oligonucleotide comprising:

A) a human tRNA structural gene sequence comprising no more than twenty 3' flanking residues and no 5' flanking residues, said sequence encoding an anticodon region for pairing with mRNA;

B) a total length of less than 150 nucleotides;

C) an anticodon sequence which has been modified to recognize a codon different from that which is originally recognized, wherein said anticodon is one which will pair with said nonsense mutation and said tRNA structural gene sequence encodes an amino acid which is deleted by said nonsense mutation.

Claim 23 (Currently amended): The ~~oligonucleotide~~ method of claim 22 wherein said anticodon region encodes an nonsense mutation selected from the group consisting of: amber (TAG), ochre (UAA) and opal (UGA).

Claim 24 (Currently amended): The ~~oligonucleotide~~ method of claim 22 wherein said tRNA structural gene sequence encodes a serine tRNA.

Claim 25 (Currently amended): The ~~oligonucleotide sequence~~ method of claim 22 wherein said tRNA structural gene sequence encodes an arginine tRNA.

Claim 26 (Currently amended): The ~~oligonucleotide~~ method of claim 22 wherein said oligonucleotide has a sequence selected from the group consisting of SEQ ID NOS:1-10, their complements ~~and their functional equivalents~~.

Claim 27 (Original): A method for introducing site-specific mutation to a translated protein comprising:

introducing to said cell a synthetic suppressor tRNA encoded by the sequence of claim 1.

Claim 28 (Original): A method for designing a synthetic suppressor tRNA comprising:

A) identifying a tRNA sequence of interest;

B) identifying the anticodon of said tRNA sequence;

C) designing an alternate anticodon sequence such that a different amino acid is translated in relation to the said anticodon than would normally be;

(D) synthesizing an oligonucleotide comprising:

a) a human tRNA structural gene sequence comprising no more than twenty 3' flanking residues and no 5' flanking residues, said sequence encoding an anticodon region for pairing with mRNA;

b) a total length of less than 150 nucleotides;

c) an anticodon sequence which has been modified to recognize a codon different from that which is originally recognized, wherein said anticodon is one which will pair with said nonsense mutation and said tRNA structural gene sequence encodes an amino acid which is deleted by said nonsense mutation.

Claim 29 (Original): The oligonucleotide of claim 28 wherein said anticodon region encodes an nonsense mutation selected from the group consisting of:

amber (TAG), ochre (UAA) and opal (UGA).

Claim 30 (Original): The oligonucleotide of claim 28 wherein said tRNA structural gene sequence encodes a serine tRNA.

Claim 31 (Original): The oligonucleotide sequence of claim 28 wherein said tRNA structural gene sequence encodes an arginine tRNA.

Claim 32 (Original): A method of treating genetic disease in animals comprising:

introducing to said animal a suppressor tRNA sequence, said tRNA sequence comprising:

A) a human tRNA structural gene sequence comprising no more than twenty 3' flanking residues and no 5' flanking residues, said sequence encoding an anticodon region for pairing with mRNA;

B) a total length of less than 150 nucleotides;

C) an anticodon sequence which has been modified to recognize a codon different from that which is originally recognized.

Claim 33 (Currently amended): The ~~oligonucleotide~~ method of claim 32 wherein said anticodon region encodes an nonsense mutation selected from the group consisting of:

amber (TAG), ochre (UAA) and opal (UGA).

Claim 34 (Currently amended): The ~~oligonucleotide~~ method of claim 32 wherein said tRNA structural gene sequence encodes a serine tRNA.

Claim 35 (Currently amended): The ~~oligonucleotide~~ method of claim 32 wherein said tRNA structural gene sequence encodes an arginine tRNA.

Claim 36 (Currently amended): The ~~oligonucleotide~~ method of claim 32 wherein said oligonucleotide has a sequence selected from the group consisting of SEQ ID NOS:1-10, their complements ~~and their functional equivalents~~.

Claim 37 (Original): The method of claim 32 wherein said disease is Xeroderma Pigmentosum.

Claim 38 (Original): A method of monitoring transduction of cells comprising:

introducing to said cells and oligonucleotide vector comprising a reporter gene said reporter gene having been inactivated by introduction of a nonsense mutation;

introducing to said cells a suppressor tRNA sequence according to claim 1; and

assaying for reactivation of the reporter gene.

Claim 39 (Original): The method of claim 38 wherein said reporter gene is selected form the group consisting of: chloramphenicol acetyl transferase and green fluorescent protein.